SEQUENCE LISTING

<110> Eli Lilly and Company

<120> Erythropoietic Compounds

<130> X-12553

<140> US 09/856,451
<141> 2001-05-22

<150> PCT/US99/27801
<151> 1999-11-23

<160> 4

<170> PatentIn version 3.2

<210> 1
<211> 168
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa at position 1 is absent or Met;

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa at position 2 is absent or is Ala, Cys, Asp, Glu, Phe, Gly, His, Ile, Leu, Met, Asn, Gln, Arg, Ser, Thr, Val, Trp, or Tyr

<220>
<221> MISC_FEATURE
<222> (26)..(26)
<223> Xaa at position 26 is Asn, Lys or Glu;

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Xaa at position 40 is Asn, Lys or Glu;

<220>
<221> MISC_FEATURE
<222> (78)..(78)
<223> Xaa at position 78 is Arg or Glu;

<220>
<221> MISC_FEATURE
<222> (85)..(85)
<223> Xaa at position 85 is Asn, Lys or Glu;

<220>
<221> MISC_FEATURE
<222> (90)..(90)
<223> Xaa at position 90 is Trp, Lys, Pro, or Arg;

<220>
<221> MISC_FEATURE
<222> (128)..(128)
<223> Xaa at position 128 is Ser, Thr, Lys or Glu;

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<220>
<221>   MISC_FEATURE
<222>   (141)..(141)
<223>   Xaa at position 141 is Arg or Glu;

<220>
<221>   MISC_FEATURE
<222>   (156)..(156)
<223>   Xaa at position 156 is Lys or Glu; and

<220>
<221>   MISC_FEATURE
<222>   (168)..(168)
<223>   Xaa at position 168 is Arg, absent, or any other amino acid.

<400>   1
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Xaa Xaa Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg
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Tyr Leu Leu Glu Ala Lys Glu Ala Glu Xaa Ile Thr Thr Gly Cys Ala
            20              25              30


Glu His Cys Ser Leu Asn Glu Xaa Ile Thr Val Pro Asp Thr Lys Val
        35              40              45


Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu
    50              55              60


Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Xaa Gly Gln
65              70              75              80


Ala Leu Leu Val Xaa Ser Ser Gln Pro Xaa Glu Pro Leu Gln Leu His
            85              90              95


Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg
            100             105             110


Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Xaa
        115             120             125


Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Xaa Lys Leu Phe
    130             135             140


Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Xaa Leu Tyr Thr Gly
145             150             155             160


Glu Ala Cys Arg Thr Gly Asp Xaa
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<210>   2
<211>   193
<212>   PRT
<213>   homo sapiens
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<400> 2

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Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1               5                  10              15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
            20                  25              30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
        35                  40                  45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
    50                  55                  60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65                  70                  75                  80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
                85                  90                  95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
            100                 105                 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
        115                 120                 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
    130                 135                 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145                 150                 155                 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
                165                 170                 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
            180                 185                 190

Arg
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<210>   3
<211>   498
<212>   DNA
<213>   homo sapiens

<400>   3
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gttccggaca ccaaagttaa cttctacgct tggaaacgta tggaagttgg tcagcaggct   180
gttgaagttt ggcagggtct ggctctgctg tccgaagctg ttctgcgtgg tcaggctctg   240
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ctggttaact cctcccagcc gtgggaaccg ctgcagctgc acgttgacaa agctgtttcc      300

ggtctgcgtt ccctgaccac cctgctgcgt gctctgggtg ctcagaaaga agctatctcc      360

ccgccggacg ctgcttccgc tgctccgctg cgtaccatca ccgctgacac cttccgtaaa      420

ctgttccgtg tttactccaa cttcctgcgt ggtaaactga aactgtacac cggtgaagct      480

tgccgtaccg gtgactga                                                    498
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<210> 4
<211> 165
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 4

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Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
1               5                   10                  15


Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
            20                  25                  30


Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
        35                  40                  45


Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
    50                  55                  60


Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
65                  70                  75                  80


Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
                85                  90                  95


Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
            100                 105                 110


Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
            115                 120                 125


Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
    130                 135                 140


Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
145                 150                 155                 160


Cys Arg Thr Gly Asp
                165
```